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14. ABSTRACT

The aim of the proposed study is to test the hypothesis that the Fragile X mental retardation protein (FMRP) prevents/resolves R loop formation to maintain genome stability. Specifically we propose that stable R loop formation impedes replication fork progression, resulting in DNA double strand breaks (DSBs), and that FMRP functions to prevent such replication-trancription conflict. We have performed three biological replicate experiments to rigorously test if the Fragile X cell line produces more DSBs than the normal control. We also developed a yeast-based recombination assay to directly test the proposed function of FMRP in R loop prevention/resolution. Finally, we performed a ChIP-seq experiment to identify the chromatin binding sites of FMRP. We are working towards obtaining a short list of genes with overlapping DSBs, R loop forming sites and FMRP-binding sites. Potential disease-correlation of these genes will then be assessed.

15. SUBJECT TERMS

FMRP; Fragile X; Genome instability; DNA double strand breaks; R loops; Break-seq; ChIP-seq

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1. Introduction

The proposed research project addresses the FY14 PRMRP Topic Area, Fragile X syndrome (FXS). FXS is responsible for the most common form of hereditary mental retardation in the world. Previous studies have established that in most cases FXS is caused by the absence of a protein named FMRP. It is generally believed that FMRP functions in regulating protein production of specific gene targets in the cytoplasm. However, we know that FMRP shuttles between the nucleus and the cytoplasm. To this date, the potential functions of FMRP in the nucleus have not been well examined. We had made a chance discovery that fragile X cells lacking FMRP show high level of chromosome breaks specifically at DNA sequences that are prone to form hybrid molecules of DNA and RNA, called R loops, during gene transcription.

This finding led us to propose that FMRP binds to its substrates directly on the chromatin (in the nucleus) and ensures that during their transcription the DNA templates do not form stable R loops. R loops are impediments to the DNA replication machinery and upon replication-transcription collision chromosomes are more prone to breakage, ultimately affecting gene expression and/or protein production of genes near the chromosome breaks (fragile sites). We proposed to directly test this hypothesis by querying the genome for FMRP binding sites. We sought to identify those specific gene substrates of FMRP with overlapping DNA double strand breaks and R loop forming sites that we deem the most probable FXS-associated genes. Thus, through these studies we hope to provide novel insights into the mechanisms of FXS pathology and enable the development of disease intervention.

In this progress report spanning July 2015 to July 2016, I will discuss the specific experiments and conclusions within each of the three aims we proposed. In summary, we have performed several biological replicate experiments to systematically map chromosome fragile sites in the Fragile X and normal control cell lines. Our results confirmed the original finding that Fragile X cell line produces more fragile sites than the normal control. We also identified chromatin-binding sites of FMRP. We examined the correlation between R loop forming sites with both fragile sites and FMRP binding sites. The results are discussed in details below.

2. Keywords

Fragile X syndrome (FXS)

Fragile X mental retardation protein (FMRP)

Genome instability

DNA double strand breaks (DSBs)

R loops (DNA:RNA hybrids)

Break-seq

ChIP-seq

3. Accomplishments

- **What were the major goals of the project?**

  We proposed three major goals for this study listed as follows:

  1) Validate the co-localized R-loop formation and chromosome fragility in Fragile X cells, particularly at the brain-expressed genes, by ChIP-seq (detecting DNA:RNA hybrids) and Break-seq (detection DNA double strand breaks, DSBs), respectively.
  2) Determine the genomic binding sites of FMRP using ChIP-seq.
  3) Examine potential changes of gene expression and protein levels of the putative FXS-associated genes in fragile X cells compared to normal cells.

- **What was accomplished under these goals?**

  Below I list the experiments and conclusions for each goal in the same order as listed above:

  1) We performed **three** biological replicate experiments of Break-seq in Fragile X cells compared to normal control cells to validate the observed correlation between DSBs and R-loop forming sites. In these experiments we induced DNA replication stress by varying concentrations of aphidicolin, a DNA polymerase inhibitor, to ascertain potentially different chromosome breakage profiles. All samples were treated with equal volumes of the vehicle, dimethylsulfonate. We also performed Break-seq on untreated samples (no aphidicolin and no vehicle) as controls. Finally, we compared cells harvested at the end of the 24-hour exposure to aphidicolin with or without metaphase arrest by colcemid (typically employed in cytological studies with metaphase chromosome spread preparations). The varying conditions of the experiments are summarized in Table 1 (no treatment controls are omitted in this table). These culture conditions represent the most comprehensive

Table 1. Summary of Break-seq experiments.

Biological replicate No.	Sample index	Aphidicolin concentration (μM)	Colcemid ("-" indicates not added, "+" added)
1 (BH collection)	AMc121614	0, 0.03, 0.3	-
2 (AC collection)	AMc051915	0, 0.03, 0.3	-
3 (AC collection)	AMc050916	0, 0.03, 0.3, 0.6, 1.5	-/+

design for genome-wide mapping of chromosome breaks to the best of our knowledge).

These experiments led to the following conclusions. **First**, our results confirmed that the Fragile X cells indeed accumulate more DSBs than normal control under replication stress. **Second**, it appeared that different concentrations of aphidicolin produced different spectra of DSBs (a more definitive conclusion is underway as the third biological replicate experiment is being analyzed). We reasoned that the gene expression patterns are also different with increasing drug concentration, thus producing R loop formation at different sites in the genome. Moreover, our cellular fractionation studies showed dynamic changes of the nuclear localization of FMRP (Fig. 1): while moderately high aphidicolin concentration increases FMRP nuclear localization, further increase of aphidicolin seemed inhibitory for this process.

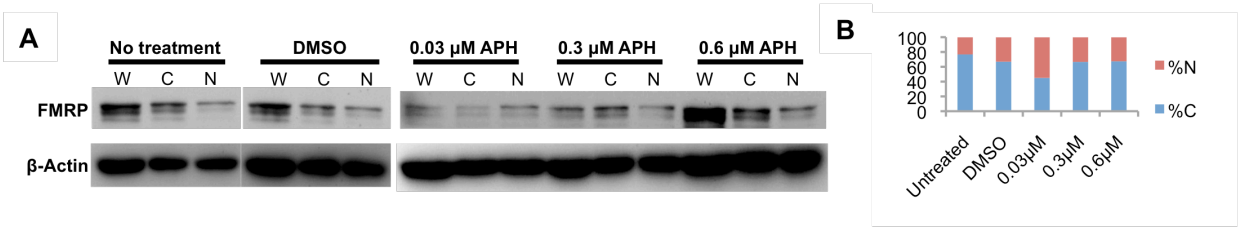

Figure 1. **(A)** Western blot analysis of subcellular localization of FMRP under different drug treatment. W, whole cell extract; C, cytoplasmic; N, nuclear. (**B**) Quantification of relative percentage of nuclear and cytoplasmic FMRP, normalized by the distribution of beta-actin, in the experiment shown in (A).

Thus, changes in the level of replication stress and nuclear retention of FMRP collectively determine the outcome of R loop regulation on the chromatin and ultimately, DNA breakage patterns. **Third**, our results indicated that DSBs are indeed correlated with the computationally predicted R-loop forming sites from the first two biological replicate experiments (the third is being analyzed). We have not yet validated these findings with DRIP-seq experiments to directly identify R-loop formation based on DNA:RNA hybrid detection.

2) We have performed a ChIP-seq experiment (biological replicates are upcoming) in the Fragile X cell line compared to a normal control (Fig. 2). We first validated using Western blots that the Fragile X cell line indeed lacks detectable FMRP expression. Then, the ChIP-seq signals from the normal control cell line were first normalized to the whole chromatin control (no

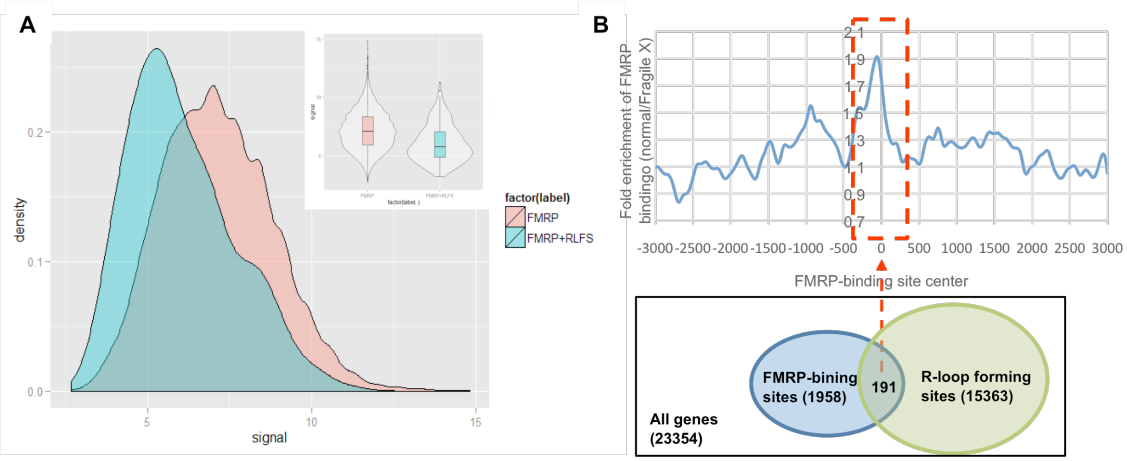

Figure 2. (**A**) Distributions of relative fractions of FMRP chromatin binding sites with (pink) or without (green) overlapping RLFSs. Inset shows the median levels of FMRP chromatin binding in the two categories. (**B**) Meta-analysis of RLFS distribution over a 6 kb window centering on the middle of all FMRP binding sites. RLFS density is relatively higher in a ± 300 bp window from the middle of a FMRP-binding site.

immunoprecipitation with anti-FMRP antibody), and then normalized against the ChIP-seq signals from the Fragile X cell line to eliminate background detection. We identified 5238 FMRP-binding sites with approximately equal division between genic and non-genic sequences. Interestingly, only 148 FMRP-binding sites overlapped with an R-loop forming site in a total of 191 genes. This result indicated that genes with co-localized FMRP binding sites and RLFSs were under-represented in the human genome ($p < 2.2E-16$ in a Fisher's exact test). Indeed, those FMRP-binding sites with overlapping R-loop forming sites showed relatively lower ChIP-seq signals or FMRP-binding levels than the genomic average FMRP-binding level). However, further analysis indicated that FMRP-binding sites were enriched in RLFS-flanking regions ((±300 bp to 3 kb from RLFS center). Therefore, these results suggest that FMRP binding sites tend to be localized to regions adjacent to R loom forming sites.

We also added an experiment to test the functional role of FMRP in R loop regulation. We reasoned that mere identification of chromatin-binding sites of FMRP does not represent a functional test of the protein in R loop regulation. Therefore, we took advantage of our expertise in yeast genetics and implemented a plasmid-based recombination assay to directly test 1) the ability of human R loop forming sequences to induce DSBs and increase recombination frequency; and 2) the ability of FMRP to reduce R loop-

induced DSB formation and recombination frequency. Our preliminary results demonstrated that FMRP expression indeed reduced recombination frequency induced by human R loop forming sequences.

3) We have not yet analyzed gene expression of putative FXS-associated genes. Once the Break-seq analysis of all experiments is completed we will short list genes with overlapping DSBs, RLFSs and FMRP-binding sites as potential FXS-associated genes. We will then examine their potentially differential gene expression or protein levels in Fragile X vs. normal cell lines.

- **What opportunities for training and professional development has the project provided?**

  This project involves two personnel: a research technician (50% effort) and a graduate student (100%). Training and professional development for the student so far are exemplified by the opportunity to assist me in writing a book chapter/mini-review of mammalian chromosome fragility.

- **How were the results disseminated to communities of interest?**

  I have presented results at three international conferences (detailed in section 6 "Products") in the form of both oral and poster presentations.

- **What do you plan to do during the next reporting period to accomplish the goals?**

  In the next reporting period we plan to complete data analyses of Break-seq experiments. We also plan to perform DRIP-seq experiments to validate *bona fide* R loop forming sites in the cell lines in our experiments. However, we place this second goal at a lower priority than the other goals in light of the results from the functional test of R loops and FMRP in yeast. We also plan to perform biological replicate experiments of ChIP-seq to validate the chromatin binding sites of FMRP. Collectively these experiments will allow us to produce a list of putative FXS-associated genes with overlapping DSBs, R loop forming sites, and FMRP-binding sites. We will study their expression levels in Fragile X cells compared to normal control in both lymphocytes as well as in neuronal cell lines derived from a mouse model of FXS.

4. IMPACT

- **What was the impact on the development of the principal discipline(s) of the project?**

  We rationalize that there are two principal disciplines of the project: genomic analysis of chromosome breakage by Break-seq and FXS disease etiology. This project represents the first application of the Break-seq methodology in the human genome. As mentioned before, our experimental design is the most comprehensive compared to studies using either conventional cytological methods (Mrasek et al 2012) or other Next-gen sequencing-based DSB mapping methods (Crosetto et al 2013; Wilson et al 2015). Specifically we tested multiple concentrations of aphidicolin as well as compared cells treated with and without colcemid. These conditions are essential to our understanding of the mechanisms of chromosome fragile site formation. Moreover, our study is the first to identify fragile sites genome-wide in the Fragile X cells. The results from our study promise to shed new light on understanding the underlying cause for FXS.

- **What was the impact on other disciplines?**

  Nothing to report.

- **What was the impact on technology transfer?**

  Nothing to report.

- **What was the impact on society beyond science and technology?**

  We believe that the results generated from our study will contribute to our understanding of FXS and other neurological disorders, and ultimately medical interventions to combat these diseases.

5. CHANGES/PROBLEMS

- **Changes in approach and reasons for change**

  The overall design of the study remains unchanged. However, as mentioned above we added an experiment where we utilized a yeast-based recombination assay to directly test the hypothesis that FMRP prevents/resolves R loop formation. This approach marks a more direct one compared to identifying chromatin-binding sites of FMRP to test the said hypothesis.

- **Actual or anticipated problems or delays and actions or plans to resolve them**

  We do not foresee problems or delays in the planned experiments.

- **Changes that had a significant impact on expenditures**

  Nothing to report.

- **Significant changes in use or care of human subjects, vertebrate animals, biohazards, and/or select agents**

  Nothing to report.

- **Significant changes in use or care of human subjects**

  Not applicable.

- **Significant changes in use or care of vertebrate animals**

  Not applicable.

- **Significant changes in use of biohazards and/or select agents**

  Nothing to report.

6. PRODUCTS

- **Publications, conference papers, and presentations**
  - Journal publication

    Nothing to report.
  - Books or other non-periodical, one-time publications

    Nothing to report.
  - Other publications, conference papers, and presentations

    June 2016, Cold Spring Harbor Asia Conference on DNA damage, Metabolism and Diseases, Suzhou, China (Poster presentation)

    Title: Global chromosome fragile site mapping by Break-seq discovers novel function of the Fragile X mental retardation protein

    February 2016, NGS Data Analysis & Informatics Conference, San Diego, California (Poster presentation)

    Title: Global detection of chromosome breakage sites by Break-seq reveals novel functions of the fragile X mental retardation protein

    September 2015, Cold Spring Harbor Conference on Eukaryotic DNA Replication and Genome Maintenance, Cold Spring Harbor, New York (Platform presentation)

    Title: Novel Function of the Fragile X Mental Retardation Protein in Genome Stability
- **Website(s) or other Internet site(s)**

  Nothing to report.
- **Technologies or techniques**

  Nothing to report.
- **Inventions, patent applications, and/or licenses**

  Nothing to report.
- **Other Products**

  Nothing to report.

7. PARTICIPANTS & OTHER COLLABORATING ORGANIZATIONS

- **What individuals have worked on the project?**

Name	Arijita Chakraborty	Andrew McCulley
Project Role	Graduate Student	Research Technician
Researcher Identifier	N.A.	N.A.
Nearest person month worked	10	4
Contribution to Project	Ms. Chakraborty performed cell culture preparations for Break-seq analysis. She also performed the ChIP-seq experiment.	Mr. McCulley assisted with Break-seq library preparations.
Funding Support	Institutional funds at Upstate Medical University	New York State Department of Health

- **Has there been a change in the active other support of the PD/PI(s) or senior/key personnel since the last reporting period?**

  The PI (W. Feng) has been rewarded an R01 grant from the National Institute of Health General Medical Sciences (scheduled to initiate in September 2016).

- **What other organizations were involved as partners?**
  - **Organization name**: A*STAR Bioinformatics Institute (academic institution, laboratory led by Dr. Vladimir Kuznetsov)
  - **Location of Organization**: Singapore
  - **Partner's contribution to the project**: Collaboration (data analysis)

8. SPECIAL REPORTING REQUIREMENTS

- **Collaborative awards**

  Not applicable.

- **Quad charts**

  Nothing to report.

9. APPENDICES

Not applicable.